

IN THE DRAWINGS:

Please replace Figure 1b with the replacement figure submitted herewith. Also submitted herewith is a marked-up copy of the original figure to locate the correction.

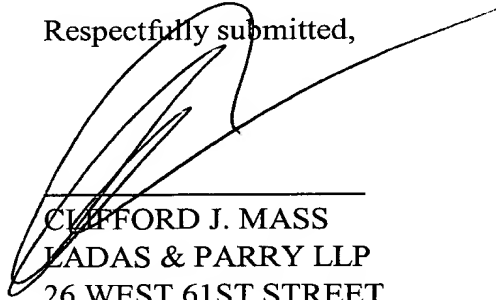
## REMARKS

The above amendatory action is taken to comply with the Official Action mailed 28 February 2006. The amendments/corrections are needed to correct the informalities noted in the Official Action. The corrections are of formal matters only and require no additional search or examination. The amendment to the specification makes clear that the sequence identified in Figure 1a of the drawings is SEQ ID NO: 5, which is already included in the Sequence Listing in the specification.

The claims have not been amended and are patentable for reasons of record. The USPTO did not previously raise objection to the drawings/specification until after the issue fee was paid, and the amendment should thereby be entered either pursuant to this request or by Examiner's Amendment.

Applicants have now fully responded to the Official Action of 28 February 2006, and respectfully request that the application be allowed to continue to issue.

Respectfully submitted,



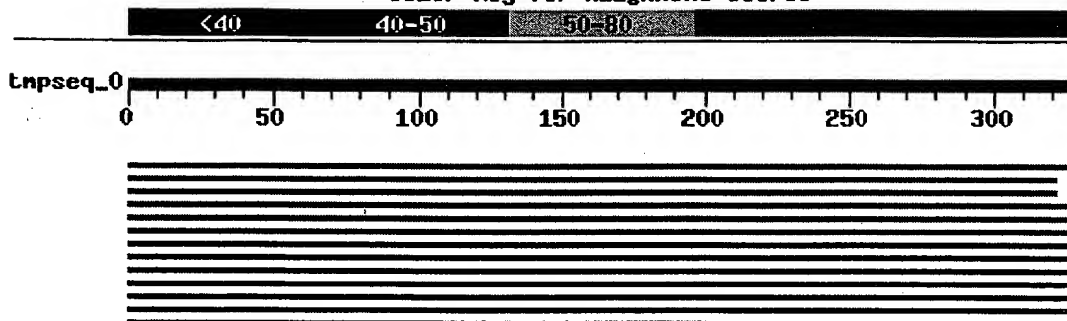
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Sequence of cytochrome b gene (328 bp) revealed from biological material of unknown origin i.e. 'adil.flesh' using primers 'mcb398' and 'mcb869'

Homology search in 'nr' database using 'BLAST'

~~http://www.ncbi.nlm.nih.gov/BLAST/~~

Color Key for Alignment Scores



Sequences producing significant alignments:	Score (bits)	E Value
gb AY005809.1  <b>Panthera pardus</b> cytochrome b gene, partial c...	603	e-170
gb AF053054.1 AF053054 <b>Panthera tigris sumatrae</b> isolate Su1...	527	e-147
gb AF053053.1 AF053053 <b>Panthera tigris tigris</b> isolate B7 mi...	527	e-147
gb AF053050.1 AF053050 <b>Panthera tigris corbetti</b> isolate C2 ...	476	e-132
gb AF053049.1 AF053049 <b>Panthera tigris corbetti</b> isolate C1 ...	476	e-132

Selection of reference animals based on above information  
and further analysis using primers 'mcb398' and 'mcb869'

Multiple sequence alignments  
using 'Autoassembler'

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225          250          275          300          325
CTAG~TCTAAT~CCTAGCAC~TCAT~ACT~AC~TCGT~C~CTATTCTCACCAGACCTGTTAGGG~GACCCC~GATAACTACAT~CCC~GCCAACCC~TI
gz2L  CTAG~TACTAAT~CCTAGCAC~TCAT~ACT~AC~TCGT~C~CTATTCTCACCAGACCTGTT~GGGAGACCCC~GATAACTACAT~C~CCC~GCCAACCC~TI
bh225l CTAG~TACTAAT~CCTAACAC~TCAT~ACT~AC~TCGT~C~CTATTCTCACCAGACCTATTAGGG~GACCCC~GATAACTACAT~C~CCC~GCCAACCC~TI
dz14sl CTAG~TACTAAT~CCTAACAC~TCAT~ACT~AC~TCGT~C~CTATTCTCACCAGACCTATTAGGG~GACGCC~GATAACTACAT~C~CCC~GCCAACCC~TI
chimss A~TTCTCT~TT~T~CCTC~CTTATCCT~AATGACAT~TAACACTATTCTCACCAGACCTCCTGGGC~GAT~CCAGACAACATATA~C~CCTAGCTAACCC~TI
gz22cl CTAG~TTCTAATTCT~AGCGC~TCAC~ACT~AC~TTGT~T~CTATTCTCACCAGACCTACTAGGA~GA~CCCTGACAA~T~TACACTCCC~GCCAACCC~TI
sbz22al CTAG~TACTAAT~CCTAACAC~TCAT~ACT~AC~TCGT~C~CTATTCTCACCAGACCTATTAGGA~GATCCC~GATAACTACAT~C~CCC~GCCAACCC~TI
humsk  CTTC~T~CT~T~CCTT~CTC~TCCTTAATGACAT~TAACACTATTCTCACCAGACCTCCTAGGC~GAC~CCAGACAATTATA~C~CCTAGCCAACCC~TI
bh220wl CTAG~TACTAAT~CCTAACAC~TCAT~ACT~AC~TCGT~C~CTATTCTCACCAGACCTATTAGGG~GACCCC~GATAACTACAT~C~CCC~GCCAACCC~TI
gz3L  CTAG~TACTAAT~CCTAGCAC~TCAT~ACT~AC~TCGT~C~CTATTCTCACCAGACCTGTT~GGGAGACCCC~GATAACTACAT~C~CCC~GCCAACCC~TI
gz1L  CTAG~TACTAAT~CCTAGCAC~TCAT~ACT~AC~TCGT~C~CTATTCTCACCAGACCTGTT~AGGAGACCCC~GATAACTACAT~C~CCT~GCCAACCC~TI
adil.flesh CTAG~TACTAAT~CCTAGCAC~TCAT~ACT~AC~TCGT~C~CTATTCTCACCAGACCTGTT~AGGAGACCCC~GATAACTACAT~C~CCT~GCCAACCC~TI

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Figure 1 b